

In the Specification

Please amend the specification as shown:

Please delete the sixth paragraph on page 9 of the English translation and replace it with the following paragraph:

Figure 2 shows a schematic representation of stem-loop structures of different lengths in heterologous nucleic acid sequences used for insertion into GFP expression constructs (SEQ ID NOS: 61-65 respectively, in order of appearance).

Please delete the first paragraph on page 10 of the English translation and replace it with the following paragraph:

Figure 4 shows a schematic representation of stem-loop structures at different positions in heterologous nucleic acid sequences used to insert GFP expression constructs (SEQ ID NOS: 66-73 respectively, in order of appearance).

Please delete the second paragraph on page 11 of the English translation and replace it with the following paragraph:

Figure 12 shows a schematic representation of two different stem-loop structures in the heterologous sequences according to the invention (SEQ ID NOS: 59 and 58 respectively, in order of appearance).

Please delete the paragraphs on page 17, line 1 to page 18, line 4 of the English translation and replace them with the following paragraphs:

Stem length 8 bp, shifted 6 bases into the GFP sequence (Residues 1-3, 13-24 and 43-60 of SEQ ID NO. 10):

HL 8 bp GFP
5'-AGG...ATGACTAGCACT...GTAAAAGGAGAAGAACTT-3'

Stem length 8 bp, shifted 9 bases into the GFP sequence (Residues 1-3, 13-27 and 46-63 of SEQ ID NO. 11):

| | | |
|-----|--|-----|
| | HL 8 bp | GFP |
| 5'- | AGG...ATGACTAGCAAACT...GTAGGAGAAGAACTTTTC | -3' |

Stem length 8 bp, shifted 12 bases into the GFP sequence (Residues 1-3, 13-30 and 49-66 of SEQ ID NO. 12):

| | | |
|-----|--|-----|
| | HL 8 bp | GFP |
| 5'- | AGG...ATGACTAGCAAAGGAACT...GTAGAAGAACTTTTCACT | -3' |

Stem length 8 bp, shifted 15 bases into the GFP sequence (Residues 1-3, 13-33 and 52-69 of SEQ ID NO. 13):

| | | |
|-----|--|-----|
| | HL 8 bp | GFP |
| 5'- | AGG...ATGACTAGCAAAGGAGAACT...GTAGAACTTTTCACTGGA | -3' |

Stem length 8 bp, shifted 18 bases into the GFP sequence (Residues 1-3, 13-36 and 55-72 of SEQ ID NO. 14):

| | | |
|-----|---|-------|
| | HL 8 bp | GFP |
| 5'- | AGG...ATGACTAGCAAAGGAGAAGAACT...GTACTTTTCACTGGAG | TT-3' |

Stem length 8 bp, shifted 21 ~~based~~ bases into the GFP sequence (Residues 1-3, 13-39 and 58-75 of SEQ ID NO. 15):

| | | |
|-----|--|----------|
| | HL 8 bp | GFP |
| 5'- | AGG...ATGACTAGCAAAGGAGAAGAACTTACT...GTATTCACTGGAG | TTGTC-3' |

Please delete the paragraph on page 24, lines 19-22 of the English translation and replace it with the following paragraph:

The sequences of the expression constructs for mutant 1 and the wild-type generated by PCR are shown in the following. The wild-type gene sequence is shown in bold type. A hexa-histidine tag (SEQ ID NO: 60) was inserted at the end of the gene using the B primer to enable detection with a specific antibody (underlined).

Please delete the paragraph on page 30, lines 15-22 of the English translation and replace it with the following paragraph:

The expressions shown in figures 6 to 9 show that DNA templates synthesized with the stem-loop structures in all cases resulted in protein synthesis whereas no protein synthesis took place with the wild-type gene. The expression of mutant 9 with the hexa-histidine sequence (SEQ ID NO: 60) is not quite as good as that of the other AT-rich sequences but has the advantage that the protein that is formed can be purified on Ni-NTA chelate columns by means of this six histidine residue (SEQ ID NO: 60) label. Even in the case of the GFP gene which is a gene that is in any case expressed well, the stem-loop constructs resulted in an increase in yield.

Please delete the paragraph on page 31, lines 13-18 of the English translation and replace it with the following paragraph:

For this a new stem-loop (loop') having the sequence CAG.ACA.AAT.AGA.TAT. TTG.TCT.GTA (SEQ ID NO: 58) ($G = -9.8$ kcal/mol and a stem length of 9 base pairs) was combined with the AT-rich sequence of mutant 1 instead of the original stem-loop sequence CTG.CAC.GTG.ATC.GTG.CAG (SEQ ID NO: 59) ($G = -9.8$ kcal/mol and a stem length of 7 base pairs) for the examples survivin, CIITA and 1049. The two structures are shown in figure 12.

Please replace the written Sequence Listing previously submitted with the national lodging on 09 June 2005, following page 32 of the English translation (14 pages), with the amended Sequence Listing submitted concurrently herewith (20 pages).